

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Chicheportiche, Yves
Browning, Jeffrey L.
- (ii) TITLE OF INVENTION: A TUMOR NECROSIS FACTOR RELATED LIGAND
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BIOGEN, INC.
 - (B) STREET: 14 CAMBRIDGE CENTER
 - (C) CITY: CAMBRIDGE
 - (D) STATE: MA
 - (E) COUNTRY: US
 - (F) ZIP: 02142
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: not yet assigned
 - (B) FILING DATE: 07-May-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: FLYNN, KERRY A.
 - (B) REGISTRATION NUMBER: 33,693
 - (C) REFERENCE/DOCKET NUMBER: A003 PCT CIP
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 679-3583
 - (B) TELEFAX: (617) 679-2838

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: TNF family related protein
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

G GTG CTG AGC CTG GGC CTG GCG CTG GCC TGC CTT GGC CTC CTG CTG
46
Val Leu Ser Leu Gly Leu Ala Leu Ala Cys Leu Gly Leu Leu Leu
1 5 10 15

GTC GTG GTC AGC CTG GGG AGC TGG GCA ACG CTG TCT GCC CAG GAG CCT
94
Val Val Val Ser Leu Gly Ser Trp Ala Thr Leu Ser Ala Gln Glu Pro
20 25 30

TCT CAG GAG GAG CTG ACA GCA GAG GAC CGC CGG GAG CCC CCT GAA CTG
142
Ser Gln Glu Glu Leu Thr Ala Glu Asp Arg Arg Glu Pro Pro Glu Leu
35 40 45

AAT CCC CAG ACA GAG GAA AGC CAG GAT GTG GTA CCT TTC TTG GAA CAA
190
Asn Pro Gln Thr Glu Glu Ser Gln Asp Val Val Pro Phe Leu Glu Gln
50 55 60

CTA GTC CGG CCT CGA AGA AGT GCT CCT AAA GGC CGG AAG GCG CGG CCT
238
Leu Val Arg Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Ala Arg Pro
65 70 75

CGC CGA GCT ATT GCA GCC CAT TAT GAG GTT CAT CCT CGG CCA GGA CAG
286
Arg Arg Ala Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln
80 85 90 95

GAT GGA GCA CAA GCA GGT GTG GAT GGG ACA GTG AGT GGC TGG GAA GAG
334
Asp Gly Ala Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu
100 105 110

ACC AAA ATC AAC AGC TCC AGC CCT CTG CGC TAC GAC CGC CAG ATT GGG
382
Thr Lys Ile Asn Ser Ser Ser Pro Leu Arg Tyr Asp Arg Gln Ile Gly
115 120 125

GAA TTT ACA GTC ATC AGG GCT GGG CTC TAC TAC CTG TAC TGT CAG GTG
430
Glu Phe Thr Val Ile Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val
130 135 140

CAC TTT GAT GAG GGA AAG GCT GTC TAC CTG AAG CTG GAC TTG CTG GTG
478
His Phe Asp Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val
145 150 155

AAC GGT GTG CTG GCC CTG CGC TGC CTG GAA GAA TTC TCA GCC ACA GCA
526
Asn Gly Val Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala
160 165 170 175

GCA AGC TCT CCT GGG CCC CAG CTC CGT TTG TGC CAG GTG TCT GGG CTG
574

Ala Ser Ser Pro Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu
180 185 190

TTG CCG CTG CGG CCA GGG TCT TCC CTT CGG ATC CGC ACC CTC CCC TGG
622

Leu Pro Leu Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp
195 200 205

GCT CAT CTT AAG GCT GCC CCC TTC CTA ACC TAC TTT GGA CTC TTT CAA
670

Ala His Leu Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln
210 215 220

GTT CAC TGAGGGGCCT TGCTCTCCCA GATTCCTTAA ACTTTCCTG GCTCCAGGAG
726

Val His
225

CATCACCACA CCTCCCTACC CCACCCCCAC TCCTCCACCC CCTCGCTGCT CCTTGGTCCA
786

GTCTGTCTC TCCTCAAAGG CAGCCAGAGC TTGTTACAT GTTTCATTG CACAGACGTA
846

TCCTTGCTCT TCTTAACATC CCATCCCACC ACAACTATCC ACCTCACTAG CTCCCAAAGC
906

CCCTACTTAT CCCTGACTCC CCCACCCACT CACCCGACCA CGTGTTTATT GACTTTGTGC
966

ACCAGGCACT GAGATGGGCT GGACCTGGTG GCAGGAAGCC AGAGAACCTG GGACTAGGCC
1026

AGAAGTTCCC AACTGTGAGG GGGAAGAGCT GGGGACAAGC TCCTCCCTGG ATCCCTGTGG
1086

ATTTTGAAAA GATACTATTT TTATTATTAT TGTGACAAAA TGTAAATGG ATATTAAAGA
1146

GAATAAATCA TGATTTCTCT TC
1168

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Leu Ser Leu Gly Leu Ala Leu Ala Cys Leu Gly Leu Leu Leu Val
1 5 10 15

Val Val Ser Leu Gly Ser Trp Ala Thr Leu Ser Ala Gln Glu Pro Ser
20 25 30

Gln Glu Glu Leu Thr Ala Glu Asp Arg Arg Glu Pro Pro Glu Leu Asn

35	40	45
Pro Gln Thr Glu Glu Ser Gln Asp Val Val Pro Phe Leu Glu Gln Leu		
50	55	60
Val Arg Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Ala Arg Pro Arg		
65	70	75 80
Arg Ala Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln Asp		
	85	90 95
Gly Ala Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu Thr		
	100	105 110
Lys Ile Asn Ser Ser Ser Pro Leu Arg Tyr Asp Arg Gln Ile Gly Glu		
	115	120 125
Phe Thr Val Ile Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His		
	130	135 140
Phe Asp Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asn		
	145	150 155 160
Gly Val Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala		
	165	170 175
Ser Ser Pro Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu		
	180	185 190
Pro Leu Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala		
	195	200 205
His Leu Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val		
	210	215 220
His		
225		

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: TNF family related protein
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..852
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG TCA TTG TTA GAC TTT GAA ATT TCC GCC CGC CGG CTC CCC CTC CCC
 48
 Met Ser Leu Leu Asp Phe Glu Ile Ser Ala Arg Arg Leu Pro Leu Pro
 1 5 10 15
 CGA TCC CTC GGG TCC CGG GAT GGG GGG GCG GTG AGG CAG GCA CAG CCC
 96
 Arg Ser Leu Gly Ser Arg Asp Gly Gly Ala Val Arg Gln Ala Gln Pro
 20 25 30
 CCC GCC CCC ATG GCC GCC CGT CGG AGC CAG AGG CGG AGG GGG CGC CGG
 144
 Pro Ala Pro Met Ala Ala Arg Arg Ser Gln Arg Arg Arg Gly Arg Arg
 35 40 45
 GGG GAG CCG GGC ACC GCC CTG CTG GTC CCG CTC GCG CTG GGC CTG GGC
 192
 Gly Glu Pro Gly Thr Ala Leu Leu Val Pro Leu Ala Leu Gly Leu Gly
 50 55 60
 CTG GCG CTG GCC TGC CTC GGC CTC CTG CTG GCC GTG GTC AGT TTG GGG
 240
 Leu Ala Leu Ala Cys Leu Gly Leu Leu Leu Ala Val Val Ser Leu Gly
 65 70 75 80
 AGC CGG GCA TCG CTG TCC GCC CAG GAG CCT GCC CAG GAG GAG CTG GTG
 288
 Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu Glu Leu Val
 85 90 95
 GCA GAG GAG GAC CAG GAC CCG TCG GAA CTG AAT CCC CAG ACA GAA GAA
 336
 Ala Glu Glu Asp Gln Asp Pro Ser Glu Leu Asn Pro Gln Thr Glu Glu
 100 105 110
 AGC CAG GAT CCT GCG CCT TTC CTG AAC CGA CTA GTT CGG CCT CGC AGA
 384
 Ser Gln Asp Pro Ala Pro Phe Leu Asn Arg Leu Val Arg Pro Arg Arg
 115 120 125
 AGT GCA CCT AAA GGC CGG AAA ACA CGG GCT CGA AGA GCG ATC GCA GCC
 432
 Ser Ala Pro Lys Gly Arg Lys Thr Arg Ala Arg Arg Ala Ile Ala Ala
 130 135 140
 CAT TAT GAA GTT CAT CCA CGA CCT GGA CAG GAC GGA GCG CAG GCA GGT
 480
 His Tyr Glu Val His Pro Arg Pro Gly Gln Asp Gly Ala Gln Ala Gly
 145 150 155 160
 GTG GAC GGG ACA GTG AGT GGC TGG GAG GAA GCC AGA ATC AAC AGC TCC
 528
 Val Asp Gly Thr Val Ser Gly Trp Glu Glu Ala Arg Ile Asn Ser Ser
 165 170 175
 AGC CCT CTG CGC TAC AAC CGC CAG ATC GGG GAG TTT ATA GTC ACC CGG
 576
 Ser Pro Leu Arg Tyr Asn Arg Gln Ile Gly Glu Phe Ile Val Thr Arg
 180 185 190

GCT GGG CTC TAC TAC CTG TAC TGT CAG GTG CAC TTT GAT GAG GGG AAG
 624
 Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp Glu Gly Lys
 195 200 205

GCT GTC TAC CTG AAG CTG GAC TTG CTG GTG GAT GGT GTG CTG GCC CTG
 672
 Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asp Gly Val Leu Ala Leu
 210 215 220

CGC TGC CTG GAG GAA TTC TCA GCC ACT GCG GCC AGT TCC CTC GGG CCC
 720
 Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala Ser Ser Leu Gly Pro
 225 230 235 240

CAG CTC CGC CTC TGC CAG GTG TCT GGG CTG TTG GCC CTG CGG CCA GGG
 768
 Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu Ala Leu Arg Pro Gly
 245 250 255

TCC TCC CTG CGG ATC CGC ACC CTC CCC TGG GCC CAT CTC AAG GCT GCC
 816
 Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala His Leu Lys Ala Ala
 260 265 270

CCC TTC CTC ACC TAC TTC GGA CTC TTC CAG GTT CAC TGAGGGGCCC
 862
 Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val His
 275 280

TGGTCTCCCC ACAGTCGTCC CAGGCTGCCG GCTCCCCTCG ACAGCTCTCT GGGCACCCGG
 922

TCCCCTCTGC CCCACCCTCA GCCGCTCTTT GCTCCAGACC TGCCCCTCCC TCTAGAGGCT
 982

GCCTGGGCCT GTTCACGTGT TTTCCATCCC ACATAAATAC AGTATTCCCA CTCTTATCTT
 1042

ACAACCTCCCC CACCGCCAC TCTCCACCTC ACTAGCTCCC CAATCCCTGA CCCTTTGAGG
 1102

CCCCCAGTGA TCTCGACTCC CCCCTGGCCA CAGACCCCCA GGGCATTGTG TTTACTGTAC
 1162

TCTGTGGGCA AGGATGGGTC CAGAAGACCC CACTTCAGGC ACTAAGAGGG GCTGGACCTG
 1222

GCGGCAGGAA GCCAAAGAGA CTGGGCCTAG GCCAGGAGTT CCCAAATGTG AGGGGCGAGA
 1282

AACAAGACAA GCTCCTCCCT TGAGAATTCC CTGTGGATTT TTAAAACAGA TATTATTTTTT
 1342

ATTATTATTG TGACAAAATG TTGATAAATG G
 1373

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Leu	Leu	Asp	Phe	Glu	Ile	Ser	Ala	Arg	Arg	Leu	Pro	Leu	Pro	1	5	10	15
Arg	Ser	Leu	Gly	Ser	Arg	Asp	Gly	Gly	Ala	Val	Arg	Gln	Ala	Gln	Pro	20	25	30	
Pro	Ala	Pro	Met	Ala	Ala	Arg	Arg	Ser	Gln	Arg	Arg	Arg	Gly	Arg	Arg	35	40	45	
Gly	Glu	Pro	Gly	Thr	Ala	Leu	Leu	Val	Pro	Leu	Ala	Leu	Gly	Leu	Gly	50	55	60	
Leu	Ala	Leu	Ala	Cys	Leu	Gly	Leu	Leu	Leu	Ala	Val	Val	Ser	Leu	Gly	65	70	75	80
Ser	Arg	Ala	Ser	Leu	Ser	Ala	Gln	Glu	Pro	Ala	Gln	Glu	Glu	Leu	Val	85	90	95	
Ala	Glu	Glu	Asp	Gln	Asp	Pro	Ser	Glu	Leu	Asn	Pro	Gln	Thr	Glu	Glu	100	105	110	
Ser	Gln	Asp	Pro	Ala	Pro	Phe	Leu	Asn	Arg	Leu	Val	Arg	Pro	Arg	Arg	115	120	125	
Ser	Ala	Pro	Lys	Gly	Arg	Lys	Thr	Arg	Ala	Arg	Arg	Ala	Ile	Ala	Ala	130	135	140	
His	Tyr	Glu	Val	His	Pro	Arg	Pro	Gly	Gln	Asp	Gly	Ala	Gln	Ala	Gly	145	150	155	160
Val	Asp	Gly	Thr	Val	Ser	Gly	Trp	Glu	Glu	Ala	Arg	Ile	Asn	Ser	Ser	165	170	175	
Ser	Pro	Leu	Arg	Tyr	Asn	Arg	Gln	Ile	Gly	Glu	Phe	Ile	Val	Thr	Arg	180	185	190	
Ala	Gly	Leu	Tyr	Tyr	Leu	Tyr	Cys	Gln	Val	His	Phe	Asp	Glu	Gly	Lys	195	200	205	
Ala	Val	Tyr	Leu	Lys	Leu	Asp	Leu	Leu	Val	Asp	Gly	Val	Leu	Ala	Leu	210	215	220	
Arg	Cys	Leu	Glu	Glu	Phe	Ser	Ala	Thr	Ala	Ala	Ser	Ser	Leu	Gly	Pro	225	230	235	240
Gln	Leu	Arg	Leu	Cys	Gln	Val	Ser	Gly	Leu	Leu	Ala	Leu	Arg	Pro	Gly	245	250	255	
Ser	Ser	Leu	Arg	Ile	Arg	Thr	Leu	Pro	Trp	Ala	His	Leu	Lys	Ala	Ala	260	265	270	
Pro	Phe	Leu	Thr	Tyr	Phe	Gly	Leu	Phe	Gln	Val	His					275	280		